

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/787,126

DATE: 10/29/2001

TIME: 15:35:51

Input Set : A:\2001-10-09 3631-0108P.txt

Output Set: N:\CRF3\10292001\I787126.raw

4 <110> APPLICANT: M&E Biotech A/S
5 HALKIER, Torben
6 HAANING, Jesper
8 <120> TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
9 Activity
11 <130> FILE REFERENCE: 3631-0108P
13 <140> CURRENT APPLICATION NUMBER: US 09/787,126
C--> 14 <141> CURRENT FILING DATE: 2001-10-09 of
16 <160> NUMBER OF SEQ ID NOS: 36
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2271
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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31 aaagccgggc tccaagtcgg cgccccacgt cgaggctccg ccgcagcctc cggagttggc 120
32 cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag 180
33 cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg 229
34 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
35 1 5 10 15
36 gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277
37 Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
38 20 25 30
39 gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc 325
40 Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
41 35 40 45
42 atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc 373
43 Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
44 50 55 60
45 gtc gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata 421
46 Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
47 65 70 75
48 tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa 469
49 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu
50 80 85 90 95
51 aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta 517
52 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu
53 100 105 110
54 ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg 565
55 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val
56 115 120 125
57 caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag 613
58 Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu

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59          130          135          140
60 aaa gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag 661
61 Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys
62          145          150          155
63 ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc 709
64 Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile
65 160          165          170          175
66 cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg 757
67 Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg
68          180          185          190
69 ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata 805
70 Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile
71          195          200          205
72 gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga 853
73 Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
74          210          215          220
75 cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg 901
76 His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met
77          225          230          235
78 gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg 949
79 Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu
80 240          245          250          255
81 atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat 997
82 Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His
83          260          265          270
84 ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag 1045
85 Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu
86          275          280          285
87 gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag 1093
88 Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
89          290          295          300
90 gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat tga 1138
91 Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
92          305          310          315
93 gccccagttt ttggagtgtt atgtatttcc tggatgtttg gaaacatttt ttaaaacaag 1198
94 ccaagaaaga tgtatatagg tgtgtgagac tactaagagg catggcccca acggtacacg 1258
95 actcagtatc catgctcttg acctgttaga gaacacgcgt atttacagcc agtgggagat 1318
96 gttagactca tgggtgtgta cacaatgggt tttaaatttt gtaatgaatt cctagaatta 1378
97 aaccagattg gagcaattac ggggttgacct tatgagaaac tgcatgtggg ctatgggagg 1438
98 ggttggtccc tggatcatgtg ccccttcgca gctgaagtgg agagggtgtc atctagcgca 1498
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100 aaaaaatact ttttctaata aggagagaaa atatatgtat ttttatataa tatctaaagt 1618
101 tatatttcag atgtaatgtt ttctttgcaa agtattgtaa attatatttg tgctatagta 1678
102 tttgattcaa aatatttaaa atgtctttgc tgttgacata tttaatgttt taaatgtaca 1738
103 gacatattta actggtgcac tttgtaaatt ccttggggaa aacttgacgc taaggagggg 1798
104 aaaaaaatgt tgtttcctaa tatcaaatgc agtatatttc ttcgttcttt ttaagttaat 1858
105 agattttttc agacttgtca agcctgtgca aaaaaattaa aatggatgcc ttgaataata 1918
106 agcaggatgt tggccaccag gtgcctttca aatttagaaa ctaattgact ttagaaagct 1978
107 gacattgcca aaaaggatac ataatgggcc actgaaatct gtcaagagta gttatataat 2038

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108 tgttgaacag gtgtttttcc acaagtgccg caaattgtac cttttttttt ttttcaaaat 2098
109 agaaaagtta ttagtggttt atcagcaaaa aagtccaatt ttaatttagt aaatgttatc 2158
110 ttatactgta caataaaaac attgcctttg aatgttaatt ttttggtaca aaaataaatt 2218
111 tatatgaaaa aaaaaaaaaa agggcgggccg ctctagaggg ccctattcta tag 2271
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115 <211> LENGTH: 317
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 2
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121 1 5 10 15
122 Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
123 20 25 30
124 Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
125 35 40 45
126 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
127 50 55 60
128 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
129 65 70 75 80
130 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
131 85 90 95
132 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
133 100 105 110
134 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
135 115 120 125
136 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
137 130 135 140
138 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
139 145 150 155 160
140 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
141 165 170 175
142 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
143 180 185 190
144 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
145 195 200 205
146 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
147 210 215 220
148 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
149 225 230 235 240
150 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
151 245 250 255
152 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
153 260 265 270
154 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
155 275 280 285
156 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
157 290 295 300
158 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
159 305 310 315

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174 <223> OTHER INFORMATION: Transmembrane domain
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178 <222> LOCATION: (454)..(948)
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185 gag atg ggc agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc 96
186 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
187 20 25 30
188 gcg cct tct gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc 144
189 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
190 35 40 45
191 atg ttc ctg gcc ctc ctg ggg ctg gga ctg ggc cag gtg gtc tgc agc 192
192 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
193 50 55 60
194 atc gct ctg ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata 240
195 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
196 65 70 75 80
197 tca gaa gac agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa 288
198 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
199 85 90 95
200 aac gca ggt ttg cag gac tcg act ctg gag agt gaa gac aca cta cct 336
201 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
202 100 105 110
203 gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag 384
204 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
205 115 120 125
206 gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct cca gct 432
207 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
208 130 135 140
209 atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag 480
210 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
211 145 150 155 160
212 gcc cag cca ttt gca cac ctc acc atc aat gct gcc agc atc cca tcg 528
213 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
214 165 170 175

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215 ggt tcc cat aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg 576
216 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
217 180 185 190
218 gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg gtt aac 624
219 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
220 195 200 205
221 caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat 672
222 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
223 210 215 220
224 gaa aca tcg gga agc gta cct aca gac tat ctt cag ctg atg gtg tat 720
225 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
226 225 230 235 240
227 gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg atg aaa 768
228 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
229 245 250 255
230 gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat 816
231 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
232 260 265 270
233 tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att 864
234 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
235 275 280 285
236 agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg 912
237 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
238 290 295 300
239 acg tac ttt ggg gct ttc aaa gtt cag gac ata gac tga 951
240 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
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245 <211> LENGTH: 316
246 <212> TYPE: PRT
247 <213> ORGANISM: Mus musculus
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253 20 25 30
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255 35 40 45
256 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
257 50 55 60
258 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
259 65 70 75 80
260 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
261 85 90 95
262 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
263 100 105 110
264 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
265 115 120 125
266 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala

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VERIFICATION SUMMARY

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